

IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application, pursuant to "Amendments In A Revised Format Now Permitted", 1267 Off. Gaz. Pat. Office 106 (February 25, 2003).

Listing of Claims:

1 - 109. (canceled)

110. (currently amended) A method of manufacturing a microarray that has single exon probes that share at least one customer-identified attribute in common, comprising:

receiving data from a customer that identify at least one ~~desired~~ common probe attribute;

identifying within a database a plurality of single exon probes having the customer-~~desired~~-identified probe attribute; and then

addressably disposing said identified probes on a support substrate capable of functioning in microarray hybridization experiments,

wherein at least 50% of the probes addressably disposed on said microarray are single exon probes that include a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

111. (previously added) The method of claim 110, wherein at least 95% of the nucleic acid probes addressably disposed on said microarray include a selectively hybridizable portion of no more than one exon of said eukaryotic genome.

112. (previously added) The method of claim 110, wherein at least 50% of the single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

113. (previously added) The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

114. (previously added) The method of claim 110, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

115. (previously added) The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

116. (previously added) The method of claim 110, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

117. (previously added) The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

118 - 119. (withdrawn)

120. (previously added) The method of claim 110, wherein said eukaryotic genome averages at least two introns per gene.

121. (previously added) The method of claim 110, wherein said eukaryotic genome averages at least three introns per gene.

122. (previously added) The method of claim 110, wherein said eukaryotic genome averages at least five introns per gene.

123. (previously added) The method of claim 110, wherein said genome is a human genome.

124. (previously added) The method of claim 110, wherein said steps of receiving customer data and identifying within a database are performed by a digital computer.

125. (currently amended) The method of claim 124, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complete complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

126. (previously added) The method of claim 125, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

127 - 130. (withdrawn)